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1	GAAACTTCTCAGAGAAATGCTCCAAAACCTCAGCAGTGCTTCTGGTGGTGCATCAGTGCT	
	-----+-----+-----+-----+-----+-----+-----+-----	
	MetLeuGlnAsnSerAlaValLeuValLeuValIleSerAla	15
	TCTGCAACCCATGAGCGGAGCAGAAATGACTCTGTGAGCCCCCAGGAAATCCCGAGTGGCG	
	+-----+-----+-----+-----+-----+-----+-----+-----	
16	SerAlaThrHisGluAlaGluGlnAsnAspSerValSerProArgLysSerArgValAla	35
	GCCCAAACTCAGGCTGAAGTGGTTGCTGCCTCAACAGTGCTCTACAGGTCCGGCTCGGGG	
	+-----+-----+-----+-----+-----+-----+-----+-----	
36	AlaGlnAsnSerAlaGluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGly	55
	GCTTTTGCAATGCCCTGGAAACTCCACCTGTGACACACAGATGGGATGTATGACATCTGTAAA	
	+-----+-----+-----+-----+-----+-----+-----+-----	
56	AlaPheAlaCysLeuGluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLys	75
	TCCTTCTGTACAGCGCTGCTAAATTGACACTCAGGGGAAAGCATTCGTCAAAGAGAGC	
	+-----+-----+-----+-----+-----+-----+-----+-----	

FIG. 1A

MATCH WITH FIG. 1B

## MATCH WITH FIG.1A

```

76  SerPheLeuTyrSerAlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSer  95
      TTTAAATGCATCGCCACGGGGTCACCTCCAAAGGTCTTCCTCGCCATTCCGAGGGTGCTCC
      +-----+-----+-----+-----+-----+-----+
96  LeuLysCysIleAlaAsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSer  115
      ACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGC
      +-----+-----+-----+-----+-----+-----+
116 ThrPheGlnArgMetIleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCys  135
      AGCATCGCCAAAGCGGAACCCCTGAAGCCATCACTGAGGTGCTCCAGCTGCCCAATCACTTC
      +-----+-----+-----+-----+-----+-----+
136 SerIleAlaLysArgAsnProGluAlaIleThrGluValValGlnLeuProAsnHisPhe  155
      TCCAACAGATACTATAACAGACTTGTCGGAAGCCTGCTGGAATGTGATGAAGACACAGTC
      +-----+-----+-----+-----+-----+-----+
156 SerAsnArgTyrTyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrVal  175

```

## MATCH WITH FIG.1C

FIG.1B

MATCH WITH FIG.1B

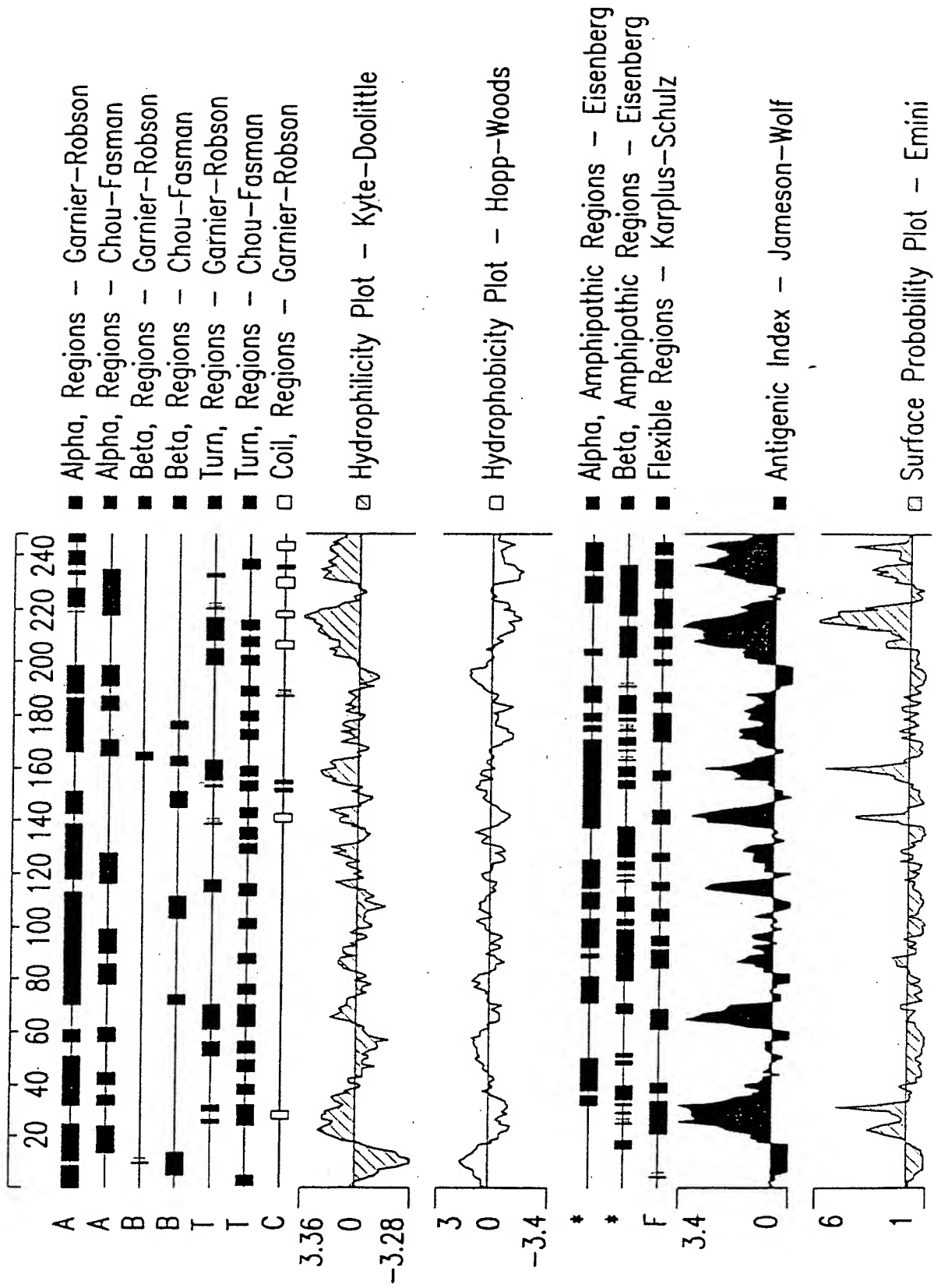
AGCACATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCAC  
 +-----+-----+-----+-----+-----+-----+-----+-----+  
 176 SerThrIleArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHis 195  
  
 ATCCTGCAGACAGACCACCTGTGCCCAACACACACCCACGAGCTGACTTCAACAGGAGACGC  
 +-----+-----+-----+-----+-----+-----+-----+-----+  
 196 IleLeuGlnThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArg 215  
  
 ACCAATGAGCCGCAGAAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCT  
 +-----+-----+-----+-----+-----+-----+-----+-----+  
 216 ThrAsnGluProGlnLysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSer 235  
  
 CCCTCCCATCAAAACGCACATCCCATGAGAGTGCATAACCAGGAGAGGT  
 +-----+-----+-----+-----+-----+-----+-----+-----+  
 236 ProSerHisIleLysArgThrSerHisGluSerAla 247

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FIG.1C

MLQNSAVLLVLVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCNLNSALQVGCFAFACL  
 ML + V ++ +A + SPR++R ++ + ++V RCLN AL VCGG FACL  
 MLAKFGLCAVFLVLGTAATFDTDPEEASPRRARESSNSPSDVARCLNGALAVGCGTFACL  
  
 ENSTCDTDGMYDICKSFLYSAAKFDTQKAFVKESLKCANGVTSKVFLAIRRCSTFQRM  
 ENSTCDTDGM+DIC+ F ++AA F+TQ GK FVKESL+CIANGVTSKVF IRRRC FQRM  
 ENSTCDTDGMHDICQLFFHTAATFNTQKTFVKESLRCIANGVTSKVFQTIIRRCGVFQRM  
  
 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDTSTIRD  
 I+EVQEECYSL++C +A+ NPEAI EVVQ+P HF NRY+ L++SLL CDE+TV+ +R  
 ISEVQEECYSRLDICGVARSNPEAIGEIVVQVPAHFPNRYYSTLLQSLACDEETVAVVRA  
  
 SLMEKIGPNMASLFHILQTDHCAQ  
 L+ ++GP+M +LF +LQ HC Q  
 GLVARLGPDMEITLFQLLQNKHCPQ 204

FIG.2



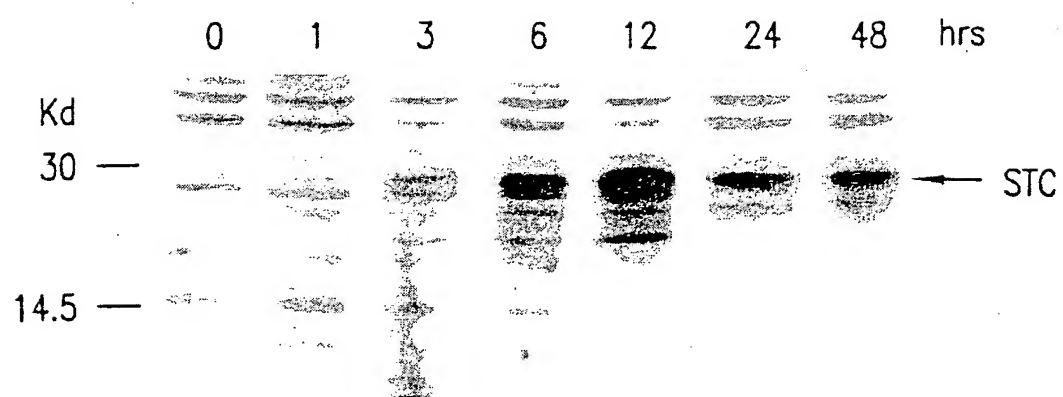


FIG.4

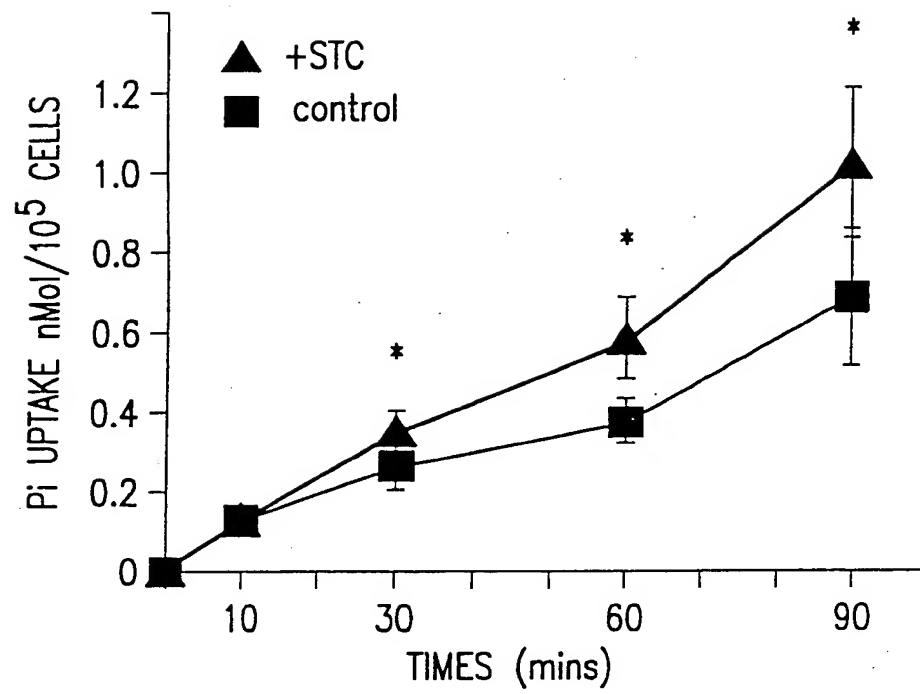


FIG.5

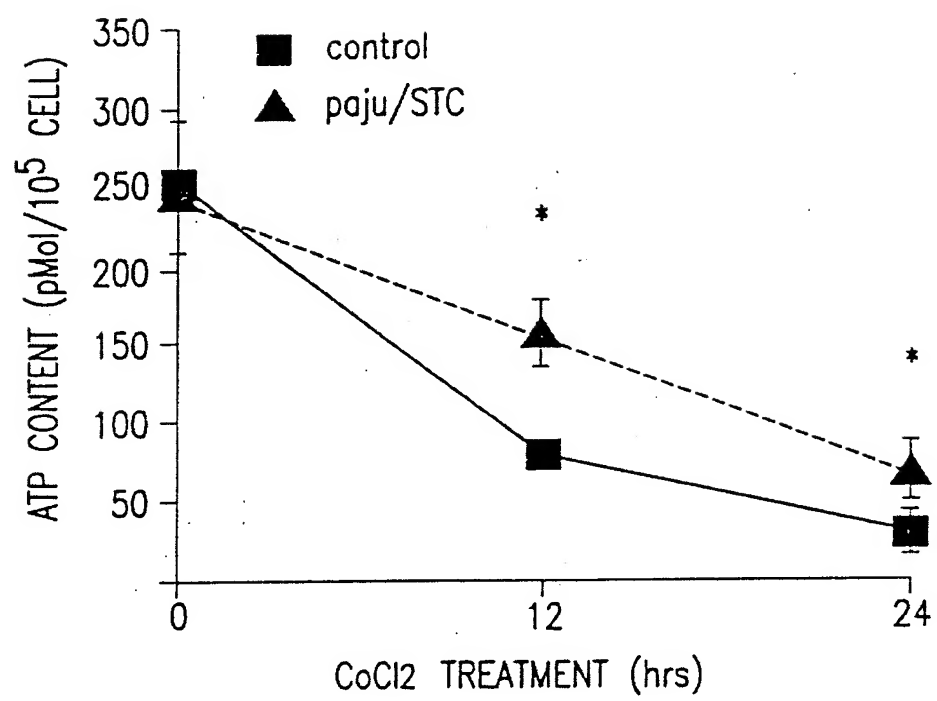


FIG.6



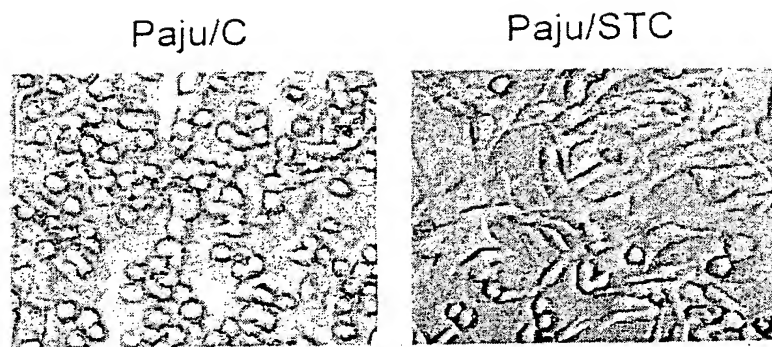


FIG.7A

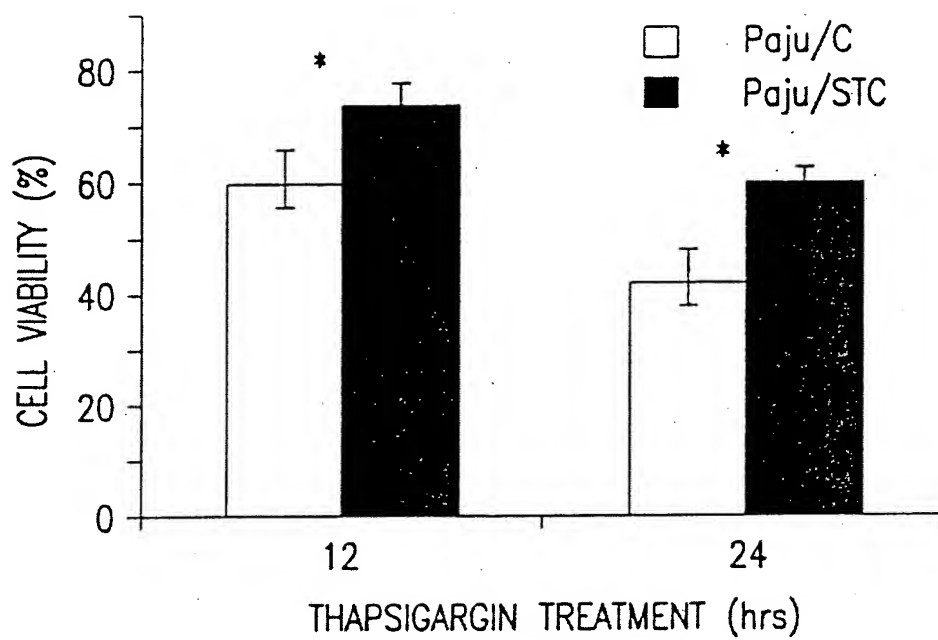


FIG.7B

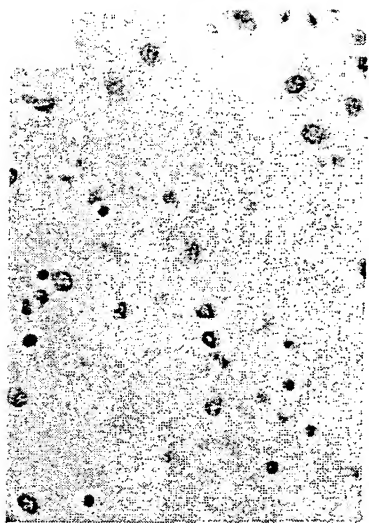


FIG. 8A



FIG. 8B

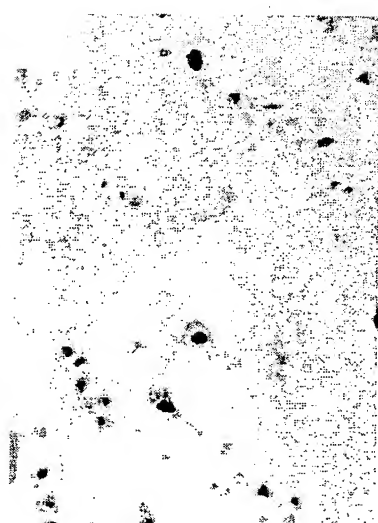


FIG. 8C

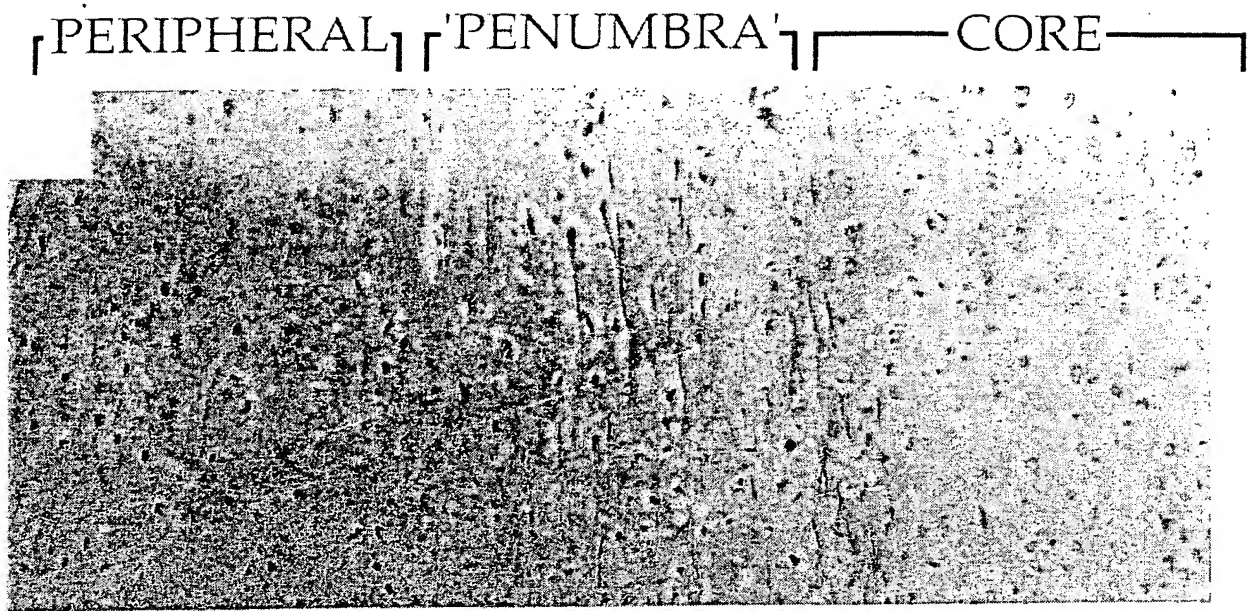


FIG.9A

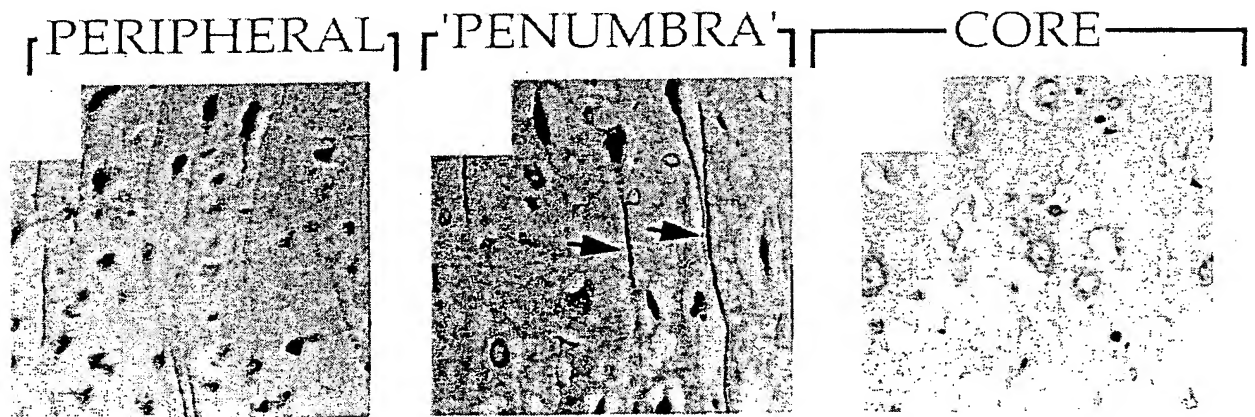


FIG.9B

FIG.9C

FIG.9D